VERSION WITH MARKINGS SHOWING CHANGES MADE

IN THE SPECIFICATION:

The first full paragraph on page 11 has been amended as follows:

According to a second aspect, the polypeptide of the invention has the ability to stimulate proliferation of endothelial cells and comprises a sequence of amino acids substantially corresponding to the amino acid sequence set out in Figure 11 (SEQ ID NO:11), or a fragment or analog thereof which has the ability to stimulate one or more of endothelial cell proliferation, differentiation, migration or survival. Preferably the polypeptides have at least 85% identity, more preferably at least 90%, and most preferably at least 95% identity to the amino acid sequence of Figure 11 [(SEQ ID NO11)] SEQ ID NO: 11, or a fragment or analog thereof having the biological activity of NZ10.

The first full paragraph on page 13 has been amended as follows:

As used herein, the term "NZ10" collectively refers to the polypeptide having the amino acid sequence set forth in Figure 11 (SEQ ID NO:11) and fragments or analogs thereof and other variants, for example, from natural isolates of the orf virus which have the biological activity of NZ10 as herein defined. Those skilled in the art will recognize that there is considerable latitude in amino acid sequence charges which can occur naturally or be engineered without affecting biological activity of the polypeptide. It is preferred that the variant polypeptides be at least 80%, more preferably be at least 90%, and most preferably at least 95% identical to the amino acid sequence of Figure 11 (SEQ ID NO:11). Percent sequence identity is determined by conventional methods. See, for example, Altschul *et al*, Bull. Math. Bio., 1986 48 603-616 and Henikoff and Henikoff, Proc. Natl. Acad. Sci. USA, 1992 89 10915-10919.

The first full paragraph on page 14 has been amended as follows:

Such variant forms of ORFV2-VEGF or NZ10 can be prepared by targeting non-essential regions of the ORFV2-VEGF or NZ10 polypeptide for modification. Other variant forms may be naturally made from related orf virus strains. These non-essential regions are expected to fall outside the strongly-conserved regions indicated in [Figure 1] Figures 1A and 1B. In particular, the growth factors of the PDGF family,

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including VEGF, are dimeric, and VEGF, VEGF-B, VEGF-C, VEGF-D, ORFV2-VEGF, PlGF, PDGF-A and PDGF-B show complete conservation of eight cysteine residues in the N-terminal domains, *ie.* the PDGF-like domains (Olofsson *et al*, 1996; Joukov *et al*, 1996). These cysteines are thought to be involved in intra- and inter-molecular disulfide bonding. In addition there are further strongly, but not completely, conserved cysteine residues in the C-terminal domains. Loops 1, 2 and 3 of each subunit, which are formed by intra-molecular disulfide bonding, are involved in binding to the receptors for the PDGF/VEGF family of growth factors (Andersson *et al*: Growth Factors, 1995 12 159-164). As noted above, the cysteines conserved in previously known members of the VEGF family are also conserved in ORFV2-VEGF.

On Page 26, the paragraph between lines 13 and 27 have been amended as follows:

[Figure 1 shows] Figures 1A and 1B show a comparative sequence alignment of the amino acid sequences of ORFV2-VEGF with other members of the VEGF family of growth factors. The deduced amino acid sequence of ORFV2-VEGF was aligned with the sequences of $VEGF_{121}$ (SEQ ID NO:3), $VEGF_{165}$ (SEQ ID NO:4), PlGF (SEQ ID NO:5), VEGF-B_{167} (SEQ ID NO:6), and truncated sequences of VEGF-C (SEQ ID NO:7) and VEGF-D (SEQ ID NO:8). The residues which show identity with ORFV2-VEGF (SEQ ID NO:2) are boxed. The conserved cysteine residues of the cystine knot motif are indicated with an asterisk. The signal sequence as determined by N-terminal sequencing is indicated by the line above the sequence. The potential sites of N- and O-linked glycosylation are indicated by a bracket and dashed line respectively. The VEGF homology domain is indicated by arrows.

The paragraph bridging pages 29 and 30 has been amended as follows:

[Figure 1 shows] Figures 1A and 1B show a comparative sequence alignment of the amino acid sequences of ORFV2-VEGF with other members of the VEGF family of growth factors. The deduced amino acid sequence of ORFV2-VEGF was aligned with the sequences of $VEGF_{121}$ (SEQ ID NO:3), $VEGF_{165}$ (SEQ ID NO:4), PlGF (SEQ ID NO:5), VEGF-B_{167} (SEQ ID NO:6), and truncated sequences of VEGF-C (SEQ ID NO:7) and VEGF-D (SEQ ID NO:8). Alignment of the predicted amino acid sequence of ORFV2-VEGF (SEQ ID NO:2) with members of the VEGF family demonstrates that ORFV2-VEGF has a high degree of sequence homology with the VEGF homology domain

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